

Best Local Similarity 100.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKARQAR 9
Db 558 AKARQAR 566

RESULT 4

AAE19387
ID AAE19387 standard; protein; 667 AA.

AC AAE19387;

DT 31-MAY-2002 (first entry)

DE Human single minded homologue 2 (SIM2) protein, long form.

KW Human; single minded homologue 2; SIM2; colon cancer; prostate cancer;

KW pancreas cancer; chromosome 21q22.2.

OS Homo sapiens.

PN WO200212565-A1.

PD 14-FEB-2002.

PF 06-AUG-2001; 2001WO-US024781.

PR 04-AUG-2000; 2000US-0223531P.

PR 22-DEC-2000; 2000US-0257965P.

PA (UFL) UNIV FLORIDA ATLANTIC.

PI Narayanan R;

DR WPI; 2002-227169/28.

DR N-PSDB; AAD30522.

PT Detecting cancer in tissue sample, involves providing tissue sample, and

PT analyzing tissue sample for presence of single minded homolog 2 marker.

XX Claim 19; Page 56; 60pp; English.

XX The invention relates to a method of detecting cancer in a tissue sample.

XX The method involves providing the tissue sample and analyzing the tissue

XX sample for the presence of a single minded homologue 2 (SIM2) nucleic

XX acid or protein, where the presence of the SIM2 marker in the tissue

XX sample indicates that the tissue sample contains cancer. The method is

XX useful for identifying compounds that modulate expression of SIM2 gene in

XX a cell. It is useful for detecting and reducing the growth of cancer such

XX as colon, prostate and pancreas cancer in an animal or mammal. The

XX present sequence is human SIM2 protein, long form. SIM2 gene is located

XX on chromosome 21q22.2

XX Sequence 667 AA;

XX Query Match 100.0%; Score 40; DB 5; Length 667;

XX Best Local Similarity 100.0%; Pred. No. 23;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKARQAR 9

Db 558 AKARQAR 566

RSULT 5

ID ABB38971 standard; peptide; 96 AA.

XX ABB38971;

XX 06-FEB-2002 (first entry)

XX Peptide #6477 encoded by human foetal liver single exon probe.

DE Human; foetal liver; gene expression; single exon nucleic acid probe.

OS Homo sapiens.

PN WO200157277-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000669.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

PD WPI; 2001-483447/52.

PF Human genome-derived single exon nucleic acid probes useful for analyzing

PF gene expression in human fetal liver.

PS Claim 27; SEQ ID NO 31606; 639pp + Sequence listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring

XX human gene expression in a sample derived from human foetal liver. The

XX single exon nucleic acid probes may be used for predicting, measuring and

XX displaying gene expression in samples derived from human fetal liver. The

XX present sequence is a peptide encoded by a single exon nucleic acid probe

XX of the invention. Note: The sequence data for this patent did not form

XX part of the printed specification, but was obtained in electronic format

XX directly from WPI at ftp.wpi.int/pub/published_pct_sequences

XX Sequence 96 AA;

XX Query Match 92.5%; Score 37; DB 4; Length 96;

XX Best Local Similarity 88.9%; Pred. No. 14;

XX Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKARQAR 9

Db 23 AKARQAR 31

RSULT 6

ID AAM32455 standard; protein; 96 AA;

XX AAM32455;

XX 18-OCT-2001 (first entry)

XX Peptide #6492 encoded by probe for measuring placental gene expression.

XX Probe; microarray; human; placenta; antenatal diagnosis;

XX genetic disorder.

XX Homo sapiens.

XX WO200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000663.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 19:02:04 ; Search time 229 Seconds
(without alignments)
27.728 Million cell updates/sec

Title: US-10-501-964-1
Perfect score: 40
Sequence: 1 AKARQANR 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: uniprot_05.80:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	40	100.0	667 1 SIM2 HUMAN	Q14190 homo sapien
2	37	92.5	80 2 Q92X88 RHIME	Q92X88 rhizobium m
3	37	92.5	516 2 Q6ZRH9 HUMAN	Q6ZRH9 homo sapien
4	36	90.0	186 2 Q5NTN3_9BACT	Q5NTN3 uncultured
5	36	90.0	562 2 Q4P8F5_USITVA	Q4P8F5 usitlago ma
6	35	87.5	135 1 RL19_XANAC	Q8PMY0 xanthomonas
7	35	87.5	135 1 RL19_XANCP	Q8PBC0 xanthomonas
8	35	87.5	135 2 Q4US85_XANCP	Q4US85 xanthomonas
9	35	87.5	167 2 Q5H389_XANOR	Q5H389 xanthomonas
10	35	87.5	469 2 Q7NK74_CHRYO	Q7NK74 chromobacter
11	35	87.5	473 2 Q4NFW2_9DELT	Q4NFW2 anaeromyxob
12	35	87.5	530 2 Q5KTI9_9BTRK	Q5KTI9 waurexilla n
13	35	87.5	599 2 Q8ABJ5_BACTN	Q8ABJ5 bacteroides
14	35	87.5	2472 2 Q14214_HUMAN	Q14214 homo sapien
15	35	87.5	3667 2 Q51QO2_HUMAN	Q51QO2 homo sapien
16	35	87.5	6669 1 NEBU_HUMAN	P20329 homo sapien
17	35	87.5	233 2 Q7NMC3_GLOVI	Q7NMC3 gloobacter
18	34	85.0	242 2 Q6ZRI0_BURMA	Q6ZRI0 burholderi
19	34	85.0	303 1 LIPO_CHRYO	Q7NUI5 chromobacter
20	34	85.0	312 2 Q9L1D3_STRCO	Q9L1D3 streptomyces
21	34	85.0	580 2 Q82XK3_NITRU	Q82XK3 nitrosomonas
22	34	85.0	716 2 Q41785_GIBZE	Q41785 gibberella
23	34	85.0	738 2 Q51J37_MAGGR	Q51J37 magnaporthe
24	34	85.0	765 2 Q8XZK9_RALSO	Q8XZK9 ralbionia s
25	33	82.5	106 2 Q5DN15_9CAUD	Q5DN15 bacteriophag
26	33	82.5	222 2 Q4NZU2_9DELT	Q4NZU2 anaeromyxob
27	33	82.5	290 2 Q4LVE1_9BURK	Q4LVE1 burholderi
28	33	82.5	359 2 Q67394_SYNTH	Q67394 symbiodact
29	33	82.5	409 2 Q8FRQ9_CORBF	Q8FRQ9 corynebacte
30	33	82.5	504 2 Q4NVJ7_9DELT	Q4NVJ7 anaeromyxob
31	33	82.5	576 2 Q551Q1_CRYNE	Q551Q1 cryptococcu

32	33	82.5	667 2 Q5KCZ6_CRYNE	Q5KCZ6 cryptococcu
33	33	82.5	696 2 Q4LML8_9BURK	Q4LML8 burholderi
34	33	82.5	698 2 Q57X86_9TRYP	Q57X86 trypanosoma
35	33	82.5	1122 2 Q4NQW1_9DELT	Q4NQW1 anaeromyxob
36	33	82.5	1178 2 Q5VOJO_ORYSA	Q5VOJO oryza sativ
37	32	80.0	68 2 Q5Q1B5_TETRU	Q5Q1B5 tetradon f
38	32	80.0	68 2 Q4RX13_TETNG	Q4RX13 tetradon n
39	32	80.0	86 2 Q89ME5_BRAJA	Q89ME5 bradyrhizob
40	32	80.0	101 2 Q4LUI9_9BURK	Q4LUI9 burholderi
41	32	80.0	110 2 Q94J97_ORYSA	Q94J97 oryza sativ
42	32	80.0	137 2 P91989_CAERL	P91989 caenorhabdi
43	32	80.0	144 2 Q53CQ0_9GAMA	Q53CQ0 maeccia fusc
44	32	80.0	177 2 Q6ZDF1_BURMA	Q6ZDF1 burholderi
45	32	80.0	209 2 P73834_SYNY3	P73834 synchocyst

ALIGNMENTS

RESULT 1
SIM2_HUMAN STANDARD; PRT: 667 AA.
ID: SIM2_HUMAN
AC Q14150; Q60766; Q15470; Q15471; Q15472; Q15473; Q15532;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DB Single-minded homolog 2.
GN Name-SIM2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA / mRNA] (ISOFORMS SIM2 AND SIM2S).
RX MEDLINE=97343329; PubMed=919934;
RA Christ R., Scott H.S., Chen H., Kudoh J., Rossier C., Minoshima S.,
Wang Y., Shimizu N., Antonarakis S.B.;
RT "Cloning of two human homologs of the Drosophila single-minded gene
SIM1 on chromosome 6q and SIM2 on 21q within the Down syndrome
chromosomal region."
RL Genome Res. 7:615-624 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Shibuya K., Kudoh J., Minoshima S., Kawasaki K., Nakatoh E.,
Shintani A., Asakawa S., Shimizu N.;
RT "Genomic sequencing of 1.2-Mb region on human chromosome 21q22.2."
RN Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;
RA Hattori W., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
Shintani A., Sasaki T., Nagamine K., Mitsuyma S., Antonarakis S.B.,
Minoshima S., Shimizu N., Nordiek G., Hornischer K., Brandt P.,
Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecher H.,
Ramer J., Beck A., Klages S., Hennig S., Resselmann L., Dagand E.,
Lehmeyer S., Borzym K., Gardiner K., Mizetic D., Francis F.,
Wehrhahn H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21."
RL Nature 405:311-319 (2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-247.
RX PubMed=8905236;
RA Oogawa K., Okano S., Kato Y., Nishimura Y., Soeda E.;
RT "A 19-kb CpG island associated with single-minded gene 2 in Down
syndrome chromosomal region."
RN DNA Res. 3:175-179 (1996).
RN [5]

RP NUCLEOTIDE SEQUENCE OF 1-58; 87-152; 183-247 AND 249-283.
 RX MEDLINE=95375794; PubMed=7647800;
 RA Chen H., Christ R., Rossier C., Goss A., Antonarakis S.E., Kudoh J.,
 RA Yamaki A., Shindoh N., Maeda H., Minoshima S., Shimizu N.;
 RT "Single-minded and Down syndrome?";
 RL Natl. Genet. 10:9-10(1995).
 [6]
 RP NUCLEOTIDE SEQUENCE [MRNA] OF 64-526.
 RC TISSUE=Fetal brain, and Muscle;
 RX MEDLINE=98163741; PubMed=9503011; DOI=10.1006/geno.1997.5146;
 RA Dahmane N., Alt Ghezala G., Gossel P., Chamoun Z.,
 RA Dufresne-Zacharia M.-C., Lopes C., Rabatel N., Gassanova-Maugendre S.,
 RA Blouin J.-L., Lebrach H., Pouetka A., Antonarakis S.E., Sinec P.-M.,
 RA Creau N., Delabar J.-M.;
 RT "Transcriptional map of the 2.5-Mb CBR-ERG region of chromosome 21
 involved in Down syndrome.";
 RL Genomics 48:12-23(1998).
 [7]
 RP NUCLEOTIDE SEQUENCE OF 87-116.
 RX MEDLINE=96016135; PubMed=7568099;
 RA Dahmane N., Charron G., Lopes C., Yagso M.-L., Maunoury C.,
 RA Decotte L., Sinec P.-M., Bloch B., Delabar J.M.;
 RT "Down syndrome-critical region contains a gene homologous to
 Drosophila sim expressed during rat and human central nervous system
 development.";
 RT Proc. Natl. Acad. Sci. U.S.A. 92:9191-9195(1995).
 [8]
 RP NUCLEOTIDE SEQUENCE OF 154-181.
 RX MEDLINE=96299750; PubMed=661114; DOI=10.1006/geno.1996.0332;
 RA Yamaki A., Noda S., Kudoh J., Shindoh N., Maeda H., Minoshima S.,
 RA Kawasaki K., Shimizu Y., Shimizu N.;
 RT "The mammalian single-minded (SIM) gene: mouse cDNA structure and
 differential expression indicate a candidate gene for Down syndrome.";
 RL Genomics 35:136-143(1996).
 [9]
 RP SUBCELLULAR LOCATION, NUCLEAR LOCALIZATION SIGNAL, AND MUTAGENESIS OF
 NLS.
 RX PubMed=14697214; DOI=10.1016/j.birc.2003.11.168;
 RA Kamaki A., Kudoh J., Shimizu N., Shimizu Y.;
 RT "A novel nuclear localization signal in the human single-minded
 protein SIM1 and SIM2";
 RL Biochem. Biophys. Res. Commun. 313:482-488(2004).
 CC -1- FUNCTION: Transcription factor that may be a master gene of CNS
 development in cooperation with Arnt. It may have pleiotropic
 effects in the tissues expressed during development.
 CC -1- SUBUNIT: Efficient DNA binding requires dimerization with another
 bHLH protein. Heterodimer of SIM2 and ARNT.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=SIM2;
 CC IsoId=Q14190-1; Sequence=Displayed;
 CC Name=SIM2S;
 CC IsoId=Q14190-2; Sequence=VSP_002148; VSP_012767;
 CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 CC -1- SIMILARITY: Contains 1 PAS (PAS-associated C-terminal) domain.
 CC -1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) domains.
 CC -1- SIMILARITY: Contains 1 Single-minded C-terminal domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; U80456; AAB62396.1; -; mRNA.
 CC EMBL; U80457; AAB62397.1; -; mRNA.
 DR EMBL; AB003185; BAA21489.1; -; Genomic DNA.
 DR EMBL; AB003185; BAA21490.1; -; Genomic DNA.
 DR EMBL; AP000697; BAA89433.1; -; Genomic DNA.
 DR EMBL; AP001726; -; NOT ANNOTATED CDS; Genomic DNA.
 DR EMBL; D85922; BAA12919.1; -; Genomic DNA.

DR EMBL; D44444; BAA07906.1; -; Genomic DNA.
 DR EMBL; D44445; BAA07907.1; -; Genomic DNA.
 DR EMBL; D44446; BAA07908.1; -; Genomic DNA.
 DR EMBL; D44447; BAA07909.1; -; Genomic DNA.
 DR EMBL; D44448; BAA07910.1; -; Genomic DNA.
 DR EMBL; A1001958; CAA05055.1; -; mRNA.
 DR EMBL; X84790; CAA59261.1; -; mRNA.
 DR EMBL; D70838; BAA11108.1; -; Genomic DNA.
 DR PIR; A58520; A58520.
 DR PIR; I78525; I78525.
 DR PIR; I78526; I78526.
 DR TRANSFAC; T04910; -;
 DR HGENC; ENSG00000159263; Homo sapiens.
 DR HGENC; HGENC:10883; SIM2.
 DR MIM; 600892; -;
 DR GO; GO:0003700; F:transcription factor activity; TAS.
 DR GO; GO:0007399; P:neurogenesis; TAS.
 DR InterPro; IPR001092; HLH basic.
 DR InterPro; IPR001067; Nuc_translocat.
 DR InterPro; IPR001610; PAS.
 DR InterPro; IPR000014; PAS.
 DR InterPro; IPR000700; PAS-assoc_C.
 DR Pfam; PF00010; HLH_1.
 DR Pfam; PF00989; PAS_1.
 DR Pfam; PF06621; SIM_C_1.
 DR PRINTS; PR00785; NCTRNSLOCATR.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAS; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS00888; HLH; 1.
 DR PROSITE; PS50113; PAS; FALSE_NEG.
 DR PROSITE; PS50112; PAS; 2.
 DR KX DNA-binding; Neurogenesis; Development;
 DR KM Alternative splicing; Nuclear protein; Repeat; Transcription;
 DR KW Transcription regulation.
 FT DOMAIN 14 54
 FT DOMAIN 77 149
 FT DOMAIN 218 288
 FT DOMAIN 292 335
 FT DOMAIN 358 661
 FT DNA BIND 1 13
 FT MOTIF 367 386
 FT VARSPPLIC 526 570
 FT FT
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Query Match 100.0%; Score 40; DB 1; Length 667;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKARQAR 9
 Db 558 AKARQAR 566

RESULT 2

Q92X88 RHIME PRELIMINARY; PRT; 80 AA.
 AC Q92X88;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Hypothetical protein SMO20074.
 GN OrderedLocustNames=RB0074; ORFNames=SMO20074;
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Plasmid psymb.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
 ON NCBI_TaxID=382;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=1021;
 RX MEDLINE=21396508; PubMed=11481431; DOI=10.1073/pnas.161294698;
 RA Flihan T.M., Weidner S., Wong K., Buhmester J., Chain P.,
 RA Vorhoefer F.J., Hernandez-Lucas I., Becker A., Cowle A., Gouzy J.,
 RA Golding B., Pehler A.;
 RT "The complete sequence of the 1,683-kb psymb megaplasmid from the N2-
 RT fixing endosymbiont Sinorhizobium meliloti."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
 DR EMBL; AL591985; CAC48474.1; -; Genomic_DNA.
 DR PIR; B95851; B95851.
 KW Complete proteome; Hypothetical protein; Plasmid.
 SQ SEQUENCE 80 AA; 8935 MW; B59C74ABAE17932 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 80;
 Best Local Similarity 88.9%; Pred. No. 20;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKARQAR 9
 Db 44 AKARQAR 52

RESULT 3

O6ZRH9 HUMAN PRELIMINARY; PRT; 516 AA.
 AC O6ZRH9;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical protein FLJ46347.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA TSSUR-Testis;
 RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
 RA Oseuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
 RA Miyakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Suzuki Y.,
 RA Sugano S., Nagahori K., Masuho Y., Nagai K., Isegai T.,
 RL Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AK128215; BAC67331.1; -; mRNA.
 SQ SEQUENCE 516 AA; 53616 MW; 1243677A7FB3F44 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 516;
 Best Local Similarity 88.9%; Pred. No. 97;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKARQAR 9
 Db 364 AKARQAR 372

RESULT 4

OSNTN3_9BACT PRELIMINARY; PRT; 186 AA.
 AC OSNTN3;
 DT 01-FEB-2005 (TREMBLrel. 29, Created)
 DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
 DE Hypothetical protein nap3-4.
 GN Name=nap3-4;
 OS uncultured bacterium.
 OC Bacteria; environmental samples.
 ON NCBI_TaxID=77133;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC PubMed=15608629; DOI=10.1038/nbt1048;
 RA Uchiyama T., Abe T., Ikemura T., Watanabe K.;
 RT "Substrate-induced gene-expression screening of environmental
 RT metagenome libraries for isolation of catabolic genes."
 RL Nat. Biotechnol. 23:88-93(2005).
 DR EMBL; AB186503; BAD0988.1; -; Genomic_DNA.
 DR InterPro; IPR004238; LEA.
 DR Pfam; PF02987; LEA_4; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 186 AA; 19238 MW; B67587D5622A37A8 CRC64;

Query Match 90.0%; Score 36; DB 2; Length 186;
 Best Local Similarity 88.9%; Pred. No. 63;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKARQAR 9
 Db 80 AKARQAR 88

RESULT 5

Q4P8F5 USTMA PRELIMINARY; PRT; 562 AA.
 AC Q4P8F5;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=UM03608.1;
 OS Ustilago maydis 521.
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 ON NCBI_TaxID=237631;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA STRAIN=521;
 RA Birren B., Nussbaum C., Abebe A., Abouelheil A., Adekoya E.,
 RA Alt-zahra M., Allen T., Allen P., Anderson M., Anderson S.,
 RA Arachchi H., Ambuster J., Bachantang P., Baldwin J., Barry A.,
 RA Bayul T., Biltsteyn B., Bloom T., Blye J., Boguslavsky L.,
 RA Bowdler M., Boukhalter B., Brunache A., Butler J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
 RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawoe T., Degray S., Dodge S., Doolley K., Dorje P.,
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
 RA Erickson J., Fatina A., Faro S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gierre S.,
 RA Gutirre A., Guyette A., Graham J., Grandbois E., Gyaltzen K., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
 RA Homan T., Horn A., Houde N., Hughes L., Hulme W., Huby B., Iliev I.,